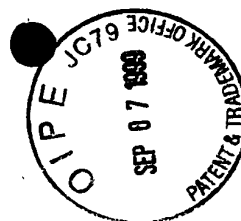


# SEQUENCE LISTING



<110> Yamamoto, Hiroaki

<120> METHOD FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUTYRIC ACID ESTER

<130> 06501/030001

<150> JP 1998-126507

<151> 1998-10-21

<150> JP 1998-300178

<151> 1998-10-21

<160> 18

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 244

<212> PRT

<213> Escherichia coli

<400> 1

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Ile	Gly	Thr	Ala	Thr	Ser	Glu	Asn	Gly	Ala	Gln	Ala	Ile	Ser	Asp	Tyr
		35					40					45			
Leu	Gly	Ala	Asn	Gly	Lys	Gly	Leu	Met	Leu	Asn	Val	Thr	Asp	Pro	Ala
	50					55					60				
Ser	Ile	Glu	Ser	Val	Leu	Glu	Lys	Ile	Arg	Ala	Glu	Phe	Gly	Glu	Val
	65				70				75					80	
Asp	Ile	Leu	Val	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Asn	Leu	Leu	Met
			85						90				95		
Arg	Met	Lys	Asp	Glu	Glu	Trp	Asn	Asp	Ile	Ile	Glu	Thr	Asn	Leu	Ser
			100					105					110		
Ser	Val	Phe	Arg	Leu	Ser	Lys	Ala	Val	Met	Arg	Ala	Met	Met	Lys	Lys
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Arg	His	Gly	Arg	Ile	Ile	Thr	Ile	Gly	Ser	Val	Val	Gly	Thr	Met	Gly
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Asn	Gly	Gly	Gln	Ala	Asn	Tyr	Ala	Ala	Ala	Lys	Ala	Gly	Leu	Ile	Gly
	145				150					155				160	
Phe	Ser	Lys	Ser	Leu	Ala	Arg	Glu	Val	Ala	Ser	Arg	Gly	Ile	Thr	Val
			165					170					175		
Asn	Val	Val	Ala	Pro	Gly	Phe	Ile	Glu	Thr	Asp	Met	Thr	Arg	Ala	Leu
			180					185					190		
Ser	Asp	Asp	Gln	Arg	Ala	Gly	Ile	Leu	Ala	Gln	Val	Pro	Ala	Gly	Arg
		195					200					205			
Leu	Gly	Gly	Ala	Gln	Glu	Ile	Ala	Asn	Ala	Val	Ala	Phe	Leu	Ala	Ser
	210					215					220				
Asp	Glu	Ala	Ala	Tyr	Ile	Thr	Gly	Glu	Thr	Leu	His	Val	Asn	Gly	Gly
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<210> 2

<211> 735

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(732)

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att ggc cgc gca att gct gaa acg ctc gca gcc cgt ggc gcg aaa gtt	96
Ile Gly Arg Ala Ile Ala Glu Thr Leu Ala Ala Arg Gly Ala Lys Val	
20 25 30	
att ggc act gcg acc agt gaa aat ggc gct cag gcg atc agt gat tat	144
Ile Gly Thr Ala Thr Ser Glu Asn Gly Ala Gln Ala Ile Ser Asp Tyr	
35 40 45	
tta ggt gcc aac ggc aaa ggt ctg atg ttg aat gtg acc gac ccg gca	192
Leu Gly Ala Asn Gly Lys Gly Leu Met Leu Asn Val Thr Asp Pro Ala	
50 55 60	
tct atc gaa tct gtt ctg gaa aaa att cgc gca gaa ttt ggt gaa gtg	240
Ser Ile Glu Ser Val Leu Glu Lys Ile Arg Ala Glu Phe Gly Glu Val	
65 70 75 80	
gat atc ctg gtc aat aat gcc ggt atc act cgt gat aac ctg tta atg	288
Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Asn Leu Leu Met	
85 90 95	
cga atg aaa gat gaa gag tgg aac gat att atc gaa acc aac ctt tca	336
Arg Met Lys Asp Glu Glu Trp Asn Asp Ile Ile Glu Thr Asn Leu Ser	
100 105 110	
tct gtt ttc cgt ctg tca aaa gcg gta atg cgc gct atg atg aaa aag	384
Ser Val Phe Arg Leu Ser Lys Ala Val Met Arg Ala Met Met Lys Lys	
115 120 125	
cgt cat ggt cgt att atc act atc ggt tct gtg gtt ggt acc atg gga	432
Arg His Gly Arg Ile Ile Thr Ile Gly Ser Val Val Gly Thr Met Gly	
130 135 140	
aat ggc ggt cag gcc aac tac gct gcg gcg aaa gcg ggc ttg atc ggc	480
Asn Gly Gly Gln Ala Asn Tyr Ala Ala Lys Ala Gly Leu Ile Gly	
145 150 155 160	
ttc agt aaa tca ctg gcg cgc gaa gtt gcg tca cgc ggt att act gta	528
Phe Ser Lys Ser Leu Ala Arg Glu Val Ala Ser Arg Gly Ile Thr Val	
165 170 175	
aac gtt gtt gct ccg ggc ttt att gaa acg gac atg aca cgt gcg ctg	576
Asn Val Val Ala Pro Gly Phe Ile Glu Thr Asp Met Thr Arg Ala Leu	
180 185 190	
agc gat gac cag cgt gcg ggt atc ctg gcg cag gtt cct gcg ggt cgc	624
Ser Asp Asp Gln Arg Ala Gly Ile Leu Ala Gln Val Pro Ala Gly Arg	
195 200 205	
ctc ggc ggc gca cag gaa atc gcc aac gcg gtt gca ttc ctg gca tcc	672
Leu Gly Gly Ala Gln Glu Ile Ala Asn Ala Val Ala Phe Leu Ala Ser	
210 215 220	

gac gaa gca gct tac atc acg ggt gaa act ttg cat gtg aac ggc ggg 720  
 Asp Glu Ala Ala Tyr Ile Thr Gly Glu Thr Leu His Val Asn Gly Gly  
 225 230 235 240

atg tac atg gtc tga 735  
 Met Tyr Met Val

<210> 3  
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 <212> DNA  
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<220>  
 <223> Artificially synthesized primer sequence

<400> 3 36  
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<210> 4  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificially synthesized primer sequence

<400> 4 32  
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<210> 5  
 <211> 248  
 <212> PRT  
 <213> Bacillus subtilis

<400> 5  
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 Gly Ile Gly Arg Ser Ile Ala Leu Ala Lys Ser Gly Ala Asn  
 20 25 30  
 Val Val Val Asn Tyr Ser Gly Asn Glu Ala Lys Ala Asn Glu Val Val  
 35 40 45  
 Asp Glu Ile Lys Ser Met Gly Arg Lys Ala Ile Ala Val Lys Ala Asp  
 50 55 60  
 Val Ser Asn Pro Glu Asp Val Gln Asn Met Ile Lys Glu Thr Leu Ser  
 65 70 75 80  
 Val Phe Ser Thr Ile Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg  
 85 90 95  
 Asp Asn Leu Ile Met Arg Met Lys Glu Asp Glu Trp Asp Asp Val Ile  
 100 105 110  
 Asn Ile Asn Leu Lys Gly Val Phe Asn Cys Thr Lys Ala Val Thr Arg  
 115 120 125  
 Gln Met Met Lys Gln Arg Ser Gly Arg Ile Ile Asn Val Ser Ser Ile  
 130 135 140  
 Val Gly Val Ser Gly Asn Pro Gly Gln Ala Asn Tyr Val Ala Ala Lys  
 145 150 155 160  
 Ala Gly Val Ile Gly Leu Thr Lys Ser Ser Ala Lys Glu Leu Ala Ser  
 165 170 175  
 Arg Asn Ile Thr Val Asn Ala Ile Ala Pro Gly Phe Ile Ser Thr Asp  
 180 185 190

Met Thr Asp Lys Leu Ala Lys Asp Val Gln Asp Glu Met Leu Lys Gln  
 195 200 205  
 Ile Pro Leu Ala Arg Phe Gly Glu Pro Ser Asp Val Ser Ser Val Val  
 210 215 220  
 Thr Phe Leu Ala Ser Glu Gly Ala Arg Tyr Met Thr Gly Gln Thr Leu  
 225 230 235 240  
 His Ile Asp Gly Gly Met Val Met  
 245

<210> 6  
 <211> 747  
 <212> DNA  
 <213> Bacillus subtilis

<220>  
 <221> CDS  
 <222> (1)...(744)

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 gga atc ggc cgc tca atc gcc ctt gct ctg gca aaa agc gga gca aat 96  
 Gly Ile Gly Arg Ser Ile Ala Leu Ala Leu Ala Lys Ser Gly Ala Asn  
 20 25 30  
 gtt gtc gtg aac tac tcc ggc aat gaa gcg aaa gca aat gaa gtg gta 144  
 Val Val Val Asn Tyr Ser Gly Asn Glu Ala Lys Ala Asn Glu Val Val  
 35 40 45  
 gat gaa atc aaa tca atg ggc aga aaa gca att gct gta aaa gcg gat 192  
 Asp Glu Ile Lys Ser Met Gly Arg Lys Ala Ile Val Lys Ala Asp  
 50 55 60  
 gta tca aat ccc gaa gat gta caa aac atg ata aaa gaa aca ttg tct 240  
 Val Ser Asn Pro Glu Asp Val Gln Asn Met Ile Lys Glu Thr Leu Ser  
 65 70 75 80  
 gtt ttt tct acg att gac att ctg gtt aat aat gcg gga att aca aga 288  
 Val Phe Ser Thr Ile Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg  
 85 90 95  
 gac aat ctc atc atg aga atg aaa gaa gac gaa tgg gat gac gtc att 336  
 Asp Asn Leu Ile Met Arg Met Lys Glu Asp Glu Trp Asp Asp Val Ile  
 100 105 110  
 aac att aac ctg aag ggt gtt ttc aac tgc aca aaa gct gtt aca aga 384  
 Asn Ile Asn Leu Lys Gly Val Phe Asn Cys Thr Lys Ala Val Thr Arg  
 115 120 125  
 caa atg atg aaa cag cgt tca ggc cgc att att aac gta tcg tct atc 432  
 Gln Met Met Lys Gln Arg Ser Gly Arg Ile Ile Asn Val Ser Ser Ile  
 130 135 140  
 gtc ggc gtc agc gga aac cct gga caa gcc aac tac gtg gct gca aaa 480  
 Val Gly Val Ser Gly Asn Pro Gly Gln Ala Asn Tyr Val Ala Ala Lys  
 145 150 155 160  
 gcc ggc gtc atc ggt tta acc aaa tct tct gct aaa gag ctc gcc agc 528  
 Ala Gly Val Ile Gly Leu Thr Lys Ser Ser Ala Lys Glu Leu Ala Ser  
 165 170 175

cga aat att acg gta aac gca ata gcg cca gga ttt atc tca act gat	576
Arg Asn Ile Thr Val Asn Ala Ile Ala Pro Gly Phe Ile Ser Thr Asp	
180 185 190	
atg aca gat aaa ctt gca aaa gac gtt caa gac gaa atg ctg aaa caa	624
Met Thr Asp Lys Leu Ala Lys Asp Val Gln Asp Glu Met Leu Lys Gln	
195 200 205	
att ccg ctc gcg cgc ttt ggt gaa cct agc gat gtc agc agt gtt gtc	672
Ile Pro Leu Ala Arg Phe Gly Glu Pro Ser Asp Val Ser Ser Val Val	
210 215 220	
acg ttc cta gct tca gag gga gct cgt tat atg aca ggc caa acg ctt	720
Thr Phe Leu Ala Ser Glu Gly Ala Arg Tyr Met Thr Gly Gln Thr Leu	
225 230 235 240	
cat att gac ggc gga atg gtg atg taa	747
His Ile Asp Gly Gly Met Val Met	
245	

<210> 7  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificially synthesized primer sequence

<400> 7  
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<210> 8  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificially synthesized primer sequence

<400> 8  
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<210> 9  
 <211> 246  
 <212> PRT  
 <213> Ralstonia eutropha

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Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln	
35 40 45	
Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp	
50 55 60	
Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly	
65 70 75 80	

Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val  
 85 90 95  
 Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn  
 100 105 110  
 Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala  
 115 120 125  
 Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln  
 130 135 140  
 Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu  
 145 150 155 160  
 His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val  
 165 170 175  
 Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys  
 180 185 190  
 Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val  
 195 200 205  
 Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu  
 210 215 220  
 Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn  
 225 230 235 240  
 Gly Gly Leu His Met Gly  
 245

<210> 10  
 <211> 741  
 <212> DNA  
 <213> *Ralstonia eutropha*

<220>  
 <221> CDS  
 <222> (1)...(738)

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 acc gcc att tgc cag cgg ctg gcc aag gat ggc ttt cgt gtg gtg gcc 96  
 Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala  
 20 25 30  
 ggt tgc ggc ccc aac tcg ccg cgc cgc gaa aag tgg ctg gag cag cag 144  
 Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln  
 35 40 45  
 aag gcc ctg ggc ttc gat ttc att gcc tcg gaa ggc aat gtg gct gac 192  
 Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp  
 50 55 60  
 tgg gac tcg acc aag acc gca ttc gac aag gtc aag tcc gag gtc ggc 240  
 Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly  
 65 70 75 80  
 gag gtt gat gtg ctg atc aac aac gcc ggt atc acc cgc gac gtg gtg 288  
 Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val  
 85 90 95  
 ttc cgc aag atg acc cgc gcc gac tgg gat gcg gtg atc gac acc aac 336  
 Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn  
 100 105 110

ctg acc tcg ctg ttc aac gtc acc aag cag gtg atc gac ggc atg gcc Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala 115 120 125	384
gac cgt ggc tgg ggc cgc atc gtc aac atc tcg tcg gtg aac ggg cag Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln 130 135 140	432
aag ggc cag ttc ggc cag acc aac tac tcc acc gcc aag gcc ggc ctg Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu 145 150 155 160	480
cat ggc ttc acc atg gca ctg gcg cag gaa gtg gcg acc aag ggc gtg His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val 165 170 175	528
acc gtc aac acg gtc tct ccg ggc tat atc gcc acc gac atg gtc aag Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys 180 185 190	576
gcg atc cgc cag gac gtg ctc gac aag atc gtc gcg acg atc ccg gtc Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val 195 200 205	624
aag cgc ctg ggc ctg ccg gaa gag atc gcc tcg atc tgc gcc tgg ttg Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu 210 215 220	672
tcg tcg gag gag tcc ggt ttc tcg acc ggc gcc gac ttc tcg ctc aac Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn 225 230 235 240	720
ggc ggc ctg cat atg ggc taa Gly Gly Leu His Met Gly 245	741

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 <213> Artificial Sequence

<220>  
 <223> Artificially synthesized primer sequence

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<210> 12  
 <211> 35  
 <212> DNA  
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<220>  
 <223> Artificially synthesized primer sequence

<400> 12  
 aacaagcttc tcgagttagc ccatatgcag gccgc 35

<210> 13  
 <211> 31  
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<213> Artificial Sequence  
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 aattctcgag taatctagag gaattctaaa a  
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 <210> 16  
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 <212> DNA  
 <213> Artificial Sequence  
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 <210> 17  
 <211> 806  
 <212> DNA  
 <213> Bacillus subtilis  
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 <221> CDS  
 <222> (12)...(794)  
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                   1                  5                  10  
 gga gct gct tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag 98  
 Gly Ala Ala Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys  
   15                  20                  25  
 gag cag gca aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg 146  
 Glu Gln Ala Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro  
   30                  35                  40                  45



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gtc caa gga gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa Val Gln Gly Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln 65 70 75	242
acg gca att aag gag ttc ggc aca ctc gat att atg att aat aat gcc Thr Ala Ile Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala 80 85 90	290
ggt ctt gaa aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg Gly Leu Glu Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp 95 100 105	338
gat aaa gtc atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt Asp Lys Val Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg 110 115 120 125	386
gaa gcg att aaa tat ttc gta gaa aac gat atc aag gga aat gtc att Glu Ala Ile Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile 130 135 140	434
aac atg tcc agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac Asn Met Ser Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His 145 150 155	482
tat gcg gca agt aaa ggc ggg ata aag ctg atg aca gaa aca tta gcg Tyr Ala Ala Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala 160 165 170	530
ttg gaa tac gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt Leu Glu Tyr Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly 175 180 185	578
gcg atc aac acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag Ala Ile Asn Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln 190 195 200 205	626
aaa gct gat gta gaa agc atg att cca atg gga tat atc ggc gaa ccg Lys Ala Asp Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro 210 215 220	674
gag gag atc gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc Glu Glu Ile Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser 225 230 235	722
tac gtc aca ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat Tyr Val Thr Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr 240 245 250	770
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<210> 18  
 <211> 261  
 <212> PRT  
 <213> Bacillus subtilis

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 1 5 10 15  
 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala  
 20 25 30  
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val  
 35 40 45  
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly  
 50 55 60  
 Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile  
 65 70 75 80  
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu  
 85 90 95  
 Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val  
 100 105 110  
 Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile  
 115 120 125  
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser  
 130 135 140  
 Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala  
 145 150 155 160  
 Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr  
 165 170 175  
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn  
 180 185 190  
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp  
 195 200 205  
 Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile  
 210 215 220  
 Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr  
 225 230 235 240  
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe  
 245 250 255  
 Gln Ala Gly Arg Gly  
 260